

SEQUENCE LISTING

(2) INFORMATION FOR SEQ ID NO: 1:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 2107
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: Human

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

GGCTCCTTAC CCACCCGAG ACTTTTTTTT GAAAGGAAAC TAGGGAGGGA GGGAGAGGGA	60
GAGAGGGAGA AAACGAAGGG GAGCTCGTCC ATCCATTGAA GCACAGTTCA CT ATG	115
	Met
	1
ATC TTA CTC ACA TTC AGC ACT GGA AGA CGG TTG GAT TTC GTG CAT CAT	163
Ile Leu Leu Thr Phe Ser Thr Gly Arg Arg Leu Asp Phe Val His His	
	5 10 15
TCG GGG GTG TTT TTC TTG CAA ACC TTG CTT TGG ATT TTA TGT GCT ACA	211
Ser Gly Val Phe Phe Leu Gln Thr Leu Leu Trp Ile Leu Cys Ala Thr	
	20 25 30
GTC TGC GGA ACG GAG CAG TAT TTC AAT GTG GAG GTT TGG TTA CAA AAG	259
Val Cys Gly Thr Glu Gln Tyr Phe Asn Val Glu Val Trp Leu Gln Lys	
	35 40 45
TAC GGC TAC CTT CCA CCG ACT AGC CCC AGA ATG TCA GTC GTG CGC TCT	307
Tyr Gly Tyr Leu Pro Pro Thr Ser Pro Arg Met Ser Val Val Arg Ser	
	50 55 60 65
GCA GAG ACC ATG CAG TCT GCC CTA GCT GCC ATG CAG CAG TTC TAT CGC	355
Ala Glu Thr Met Gln Ser Ala Leu Ala Ala Met Gln Gln Phe Tyr Gly	
	70 75 80
ATT AAC ATG ACA GGA AAA GTG GAC AGA AAC ACA ATT GAC TGG ATG AAG	403
Ile Asn Met Thr Gly Lys Val Asp Arg Asn Thr Ile Asp Trp Met Lys	
	85 90 95
AAG CCC CGA TGC GGT GTA CCT GAC CAG ACA AGA GGT AGC TCC AAA TTT	451
Lys Pro Arg Cys Gly Val Pro Asp Gln Thr Arg Gly Ser Ser Lys Phe	
	100 105 110
CAT ATT CGT CGA AAG CGA TAT GCA TTG ACA GGA CAG AAA TGG CAG CAC	499
His Ile Arg Arg Lys Arg Tyr Ala Leu Thr Gly Gln Lys Trp Gln His	
	115 120 125

002227-200460

AAG Lys 130	CAC His	ATC Ile	ACT Thr	TAC Tyr	AGT Ser 135	ATA Ile	AAG Lys	AAC Asn	GTA Val	ACT Thr 140	CCA Pro	AAA Lys	GTA Val	GGA Gly	GAC Asp 145	547
CCT Pro	GAG Glu	ACT Thr	CGT Arg	AAA Lys 150	GCT Ala	ATT Ile	CGC Arg	CGT Arg	GCC Ala 155	TTT Phe	GAT Asp	GTG Val	TGG Trp	CAG Gln 160	AAT Asn	595
GTA Val	ACT Thr	CCT Pro	CTG Leu 165	ACA Thr	TTT Phe	GAA Glu	GAA Glu	GTT Val 170	CCC Pro	TAC Tyr	AGT Ser	GAA Glu	TTA Leu 175	GAA Glu	AAT Asn	643
GGC Gly	AAA Lys	CGT Arg 180	GAT Asp	GTG Val	GAT Asp	ATA Ile	CCC Pro 185	ATT Ile	ATT Ile	TTT Phe	GCA Ala	TCT Ser 190	GGT Gly	TTC Phe	CAT His	691
GGG Gly	GAC Asp 195	AGC Ser	TCT Ser	CCC Pro	TTT Phe	GAT Asp 200	GGA Gly	GAG Glu	GGA Gly	GGA Gly	TTT Phe 205	TTG Leu	GCA Ala	CAT His	GCC Ala	739
TAC Tyr 210	TTC Phe	CCT Pro	GGA Gly	CCA Pro	GGA Gly 215	ATT Ile	GGA Gly	GGA Gly	GAT Asp	ACC Thr 220	CAT His	TTT Phe	GAC Asp	TCA Ser	GAT Asp 225	787
GAG Glu	CCA Pro	TGG Trp	ACA Thr	CTA Leu 230	GGA Gly	AAT Asn	CCT Pro	AAT Asn	CAT His 235	GAT Asp	GGA Gly	AAT Asn	GAC Asp	TTA Leu 240	TTT Phe	835
CTT Leu	GTA Val	GCA Ala	GTC Val 245	CAT His	GAA Glu	CTG Leu	GGA Gly	CAT His 250	GCT Ala	CTG Leu	GGA Gly	TTG Leu	GAG Glu 255	CAT His	TCC Ser	883
AAT Asn	GAC Asp	CCC Pro 260	ACT Thr	GCC Ala	ATC Ile	ATG Met	GCT Ala 265	CCA Pro	TTT Phe	TAC Tyr	CAG Gln	TAC Tyr 270	ATG Met	GAA Glu	CAG Gln	931
ACA Thr	CTT Leu 275	CAA Gln	CTA Leu	CCT Pro	AAT Asn	GAT Asp 280	GAT Asp	TAC Tyr	AGG Arg	CAT His	CAG Gln 285	AGA Arg	TAT Tyr	ATG Met	TCA Ser	979
CCT Pro 290	GAC Asp	AAG Lys	ATT Ile	CCT Pro	CCA Pro 295	CCT Pro	ACA Thr	AGA Arg	CCT Pro	CTA Leu 300	CCG Pro	ACA Thr	GTG Val	CCC Pro	CCA Pro 305	1027
CAC His	CGC Arg	TCT Ser	ATT Ile	CCT Pro 310	CCG Pro	GCT Ala	GAC Asp	CCA Pro	AGG Arg 315	AAA Lys	AAT Asn	GAC Asp	AGG Arg	CCA Pro 320	AAA Lys	1075
CCT Pro	CCT Pro	CGG Arg	CCT Pro 325	CCA Pro	ACC Thr	GGC Gly	AGA Arg	CCC Pro 330	TCC Ser	TAT Tyr	CCC Pro	GGA Gly	GCC Ala 335	AAA Lys	CCC Pro	1123
AAC Asn	ATC Ile	TGT Cys 340	GAT Asp	GGG Gly	AAC Asn	TTT Phe	AAC Asn 345	ACT Thr	CTA Leu	GCT Ala	ATT Ile	CTT Leu 350	CGT Arg	CGT Arg	GAG Glu	1171

ATG	TTT	GTT	TTC	AAG	GAC	CAG	TGG	TTT	TGG	CGA	GTG	AGA	AAC	AAC	AGG	1219
Met	Phe	Val	Phe	Lys	Asp	Gln	Trp	Phe	Trp	Arg	Val	Arg	Asn	Asn	Arg	
	355					360					365					
GTG	ATG	GAT	GGA	TAC	CCA	ATG	CAA	ATT	ACT	TAC	TTC	TGG	CGG	GGC	TTG	1267
Val	Met	Asp	Gly	Tyr	Pro	Met	Gln	Ile	Thr	Tyr	Phe	Trp	Arg	Gly	Leu	
370					375					380					385	
CCT	CCT	AGT	ATC	GAT	GCA	GTT	TAT	GAA	AAT	AGC	GAC	GGG	AAT	TTT	GTG	1315
Pro	Pro	Ser	Ile	Asp	Ala	Val	Tyr	Glu	Asn	Ser	Asp	Gly	Asn	Phe	Val	
				390					395					400		
TTC	TTT	AAA	GGT	AAC	AAA	TAT	TGG	GTG	TTC	AAG	GAT	ACA	ACT	CTT	CAA	1363
Phe	Phe	Lys	Gly	Asn	Lys	Tyr	Trp	Val	Phe	Lys	Asp	Thr	Thr	Leu	Gln	
		405					410						415			
CCT	GGT	TAC	CCT	CAT	GAC	TTG	ATA	ACC	CTT	GGA	AGT	GGA	ATT	CCC	CCT	1411
Pro	Gly	Tyr	Pro	His	Asp	Leu	Ile	Thr	Leu	Gly	Ser	Gly	Ile	Pro	Pro	
	420					425						430				
CAT	GGT	ATT	GAT	TCA	GCC	ATT	TGG	TGG	GAG	GAC	GTC	GGG	AAA	ACC	TAT	1459
His	Gly	Ile	Asp	Ser	Ala	Ile	Trp	Trp	Glu	Asp	Val	Gly	Lys	Thr	Tyr	
	435					440					445					
TTC	TTC	AAG	GGA	GAC	AGA	TAT	TGG	AGA	TAT	AGT	GAA	GAA	ATG	AAA	ACA	1507
Phe	Phe	Lys	Gly	Asp	Arg	Tyr	Trp	Arg	Tyr	Ser	Glu	Glu	Met	Lys	Thr	
450					455					460					465	
ATG	GAC	CCT	GGC	TAT	CCC	AAG	CCA	ATC	ACA	GTC	TGG	AAA	GGG	ATC	CCT	1555
Met	Asp	Pro	Gly	Tyr	Pro	Lys	Pro	Ile	Thr	Val	Trp	Lys	Gly	Ile	Pro	
				470					475					480		
GAA	TCT	CCT	CAG	GGA	GCA	TTT	GTA	CAC	AAA	GAA	AAT	GGC	TTT	ACG	TAT	1603
Glu	Ser	Pro	Gln	Gly	Ala	Phe	Val	His	Lys	Glu	Asn	Gly	Phe	Thr	Tyr	
			485				490					495				
TTC	TAC	AAG	GAA	GGA	GTA	TTG	GAA	ATT	CAA	ACA	ACC	AGA	TAC	TCA	AGG	1651
Phe	Tyr	Lys	Glu	Gly	Val	Leu	Glu	Ile	Gln	Thr	Thr	Arg	Tyr	Ser	Arg	
		500				505						510				
CTA	GAA	CCT	GGA	CAT	CCA	AGA	TCC	ATC	CTC	AAG	GAT	TTA	TCG	GGC	TGT	1699
Leu	Glu	Pro	Gly	His	Pro	Arg	Ser	Ile	Leu	Lys	Asp	Leu	Ser	Gly	Cys	
	515					520					525					
GAT	GGA	CCA	ACA	GAC	AGA	GTT	AAA	GAA	GGA	CAC	AGC	CCA	CCA	GAT	GAT	1747
Asp	Gly	Pro	Thr	Asp	Arg	Val	Lys	Glu	Gly	His	Ser	Pro	Pro	Asp	Asp	
530					535					540					545	
GTA	GAC	ATT	GTC	ATC	AAA	CTG	GAC	AAC	ACA	GCC	AGC	ACT	GTG	AAA	GCC	1795
Val	Asp	Ile	Val	Ile	Lys	Leu	Asp	Asn	Thr	Ala	Ser	Thr	Val	Lys	Ala	
				550					555					560		
ATA	GCT	ATT	GTC	ATT	CCC	TGC	ATC	TTG	GCC	TTA	TGC	CTC	CTT	GTA	TTG	1843
Ile	Ala	Ile	Val	Ile	Pro	Cys	Ile	Leu	Ala	Leu	Cys	Leu	Leu	Val	Leu	
			565					570					575			

002121" 2004E/60

GTT TAC ACT GTG TTC CAG TTC AAG AGG AAA GGA ACA CCC CGC CAC ATA 1891
Val Tyr Thr Val Phe Gln Phe Lys Arg Lys Gly Thr Pro Arg His Ile
580 590

CTG TAC TGT AAA CGC TCT ATG CAA GAG TGG GTG TGATGTAGGG TTTTCTTCTC 1944
Leu Tyr Cys Lys Arg Ser Met Gln Glu Trp Val
595 600 604

TTTCTTTCTT TTGCAGGAGT TTGTGGTAAC TTGAGATTCA AGACAAGAGC TGTATGCTG 2004

TTTCCTAGCT AGGAGCAGGC TTGTGGCAGC CTGATTCGGG GCTGACCTTT CAAACCAGAG 2064

GGTTGCTTGG TCCTGCACAT GAGTGGAAAT ACACTCATGG GGA 2107

(2) INFORMATION FOR SEQ ID NO: 2:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 604
(B) TYPE: Amino acid

(ii) MOLECULE TYPE: Protein

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Human

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

Met Ile Leu Leu Thr Phe Ser Thr Gly Arg Arg Leu Asp Phe Val His
1 5 10 15

His Ser Gly Val Phe Phe Leu Gln Thr Leu Leu Trp Ile Leu Cys Ala
20 25 30

Thr Val Cys Gly Thr Glu Gln Tyr Phe Asn Val Glu Val Trp Leu Gln
35 40 45

Lys Tyr Gly Tyr Leu Pro Pro Thr Ser Pro Arg Met Ser Val Val Arg
50 55 60

Ser Ala Glu Thr Met Gln Ser Ala Leu Ala Ala Met Gln Gln Phe Tyr
65 70 75 80

Gly Ile Asn Met Thr Gly Lys Val Asp Arg Asn Thr Ile Asp Trp Met
85 90 95

Lys Lys Pro Arg Cys Gly Val Pro Asp Gln Thr Arg Gly Ser Ser Lys
100 105 110

Phe His Ile Arg Arg Lys Arg Tyr Ala Leu Thr Gly Gln Lys Trp Gln
115 120 125

His Lys His Ile Thr Tyr Ser Ile Lys Asn Val Thr Pro Lys Val Gly
130 135 140

00222"2004E250

Asp 145	Pro	Glu	Thr	Arg	Lys 150	Ala	Ile	Arg	Arg	Ala 155	Phe	Asp	Val	Trp	Gln 160
Asn	Val	Thr	Pro	Leu 165	Thr	Phe	Glu	Glu	Val 170	Pro	Tyr	Ser	Glu	Leu 175	Glu
Asn	Gly	Lys	Arg 180	Asp	Val	Asp	Ile	Pro 185	Ile	Ile	Phe	Ala	Ser 190	Gly	Phe
His	Gly	Asp 195	Ser	Ser	Pro	Phe	Asp 200	Gly	Glu	Gly	Gly	Phe 205	Leu	Ala	His
Ala	Tyr 210	Phe	Pro	Gly	Pro	Gly 215	Ile	Gly	Gly	Asp	Thr 220	His	Phe	Asp	Ser
Asp 225	Glu	Pro	Trp	Thr	Leu 230	Gly	Asn	Pro	Asn	His 235	Asp	Gly	Asn	Asp	Leu 240
Phe	Leu	Val	Ala 245	Val	His	Glu	Leu	Gly	His 250	Ala	Leu	Gly	Leu	Glu 255	His
Ser	Asn	Asp	Pro 260	Thr	Ala	Ile	Met	Ala 265	Pro	Phe	Tyr	Gln	Tyr 270	Met	Glu
Gln	Thr	Leu 275	Gln	Leu	Pro	Asn	Asp 280	Asp	Tyr	Arg	His	Gln 285	Arg	Tyr	Met
Ser	Pro 290	Asp	Lys	Ile	Pro	Pro 295	Pro	Thr	Arg	Pro	Leu 300	Pro	Thr	Val	Pro
Pro 305	His	Arg	Ser	Ile	Pro 310	Pro	Ala	Asp	Pro	Arg 315	Lys	Asn	Asp	Arg	Pro 320
Lys	Pro	Pro	Arg 325	Pro	Pro	Thr	Gly	Arg	Pro 330	Ser	Tyr	Pro	Gly	Ala 335	Lys
Pro	Asn	Ile 340	Cys	Asp	Gly	Asn	Phe	Asn 345	Thr	Leu	Ala	Ile	Leu 350	Arg	Arg
Glu	Met	Phe 355	Val	Phe	Lys	Asp	Gln 360	Trp	Phe	Trp	Arg	Val 365	Arg	Asn	Asn
Arg	Val 370	Met	Asp	Gly	Tyr	Pro 375	Met	Gln	Ile	Thr	Tyr 380	Phe	Trp	Arg	Gly
Leu 375	Pro	Pro	Ser	Ile	Asp 390	Ala	Val	Tyr	Glu	Asn 395	Ser	Asp	Gly	Asn	Phe 400
Val	Phe	Phe	Lys 405	Gly	Asn	Lys	Tyr	Trp	Val 410	Phe	Lys	Asp	Thr	Thr 415	Leu
Gln	Pro	Gly	Tyr 420	Pro	His	Asp	Leu	Ile 425	Thr	Leu	Gly	Ser	Gly 430	Ile	Pro
Pro	His 435	Gly	Ile	Asp	Ser	Ala	Ile 440	Trp	Trp	Glu	Asp 445	Val	Gly	Lys	Thr

(2) INFORMATION FOR SEQ ID NO: 3:

(A) LENGTH: 20
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

20

(i) SEQUENCE CHARACTERISTICS:

(ii) MOLECULE TYPE: Other nucleic acid
Synthetic DNA

YTCRTSNTCR TCRAARTGRR HRTCYYCC

(2) INFORMATION FOR SEQ ID NO: 5:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH:	14
(B) TYPE:	Amino acid
(C) TOPOLOGY:	Linear

(ii) MOLECULE TYPE: Peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:

Gln Thr Arg Gly Ser Ser Lys Phe His Ile Arg Arg Lys Arg
1 5 10 14

(2) INFORMATION FOR SEQ ID NO: 6:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH:	14
(B) TYPE:	Amino acid
(C) TOPOLOGY:	Linear

(ii) MOLECULE TYPE: Peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:

Glu Glu Val Pro Tyr Ser Glu Leu Glu Asn Gly Lys Arg Asp
1 5 10 14

(2) INFORMATION FOR SEQ ID NO: 7:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH:	18
(B) TYPE:	Amino acid
(C) TOPOLOGY:	Linear

(ii) MOLECULE TYPE: Peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:

Pro Thr Ser Pro Arg Met Ser Val Val Arg Ser Ala Glu Thr Met Gln
1 5 10 15

Ser Ala
18

SEQUENCE LISTING

(1) GENERAL INFORMATION

- (i) APPLICANT: Motoharu SEIKI et al.
- (ii) TITLE OF INVENTION: NOVEL PROTEIN AND MONOCLONAL ANTIBODY SPECIFIC THERETO
- (iii) NUMBER OF SEQUENCES: 14
- (iv) CORRESPONDENCE ADDRESS:
(A) ADDRESSEE: Wenderoth, Lind & Ponack, L.L.P.
(B) STREET: 2033 K Street, N.W., Suite 800
(C) CITY: Washington
(D) STATE: D.C.
(E) COUNTRY: U.S.A.
(F) ZIP: 20006
- (v) COMPUTER READABLE FORM:
(A) MEDIUM TYPE: Diskette, 3.5 inch, 1.44 mb
(B) COMPUTER: IBM Compatible
(C) OPERATING SYSTEM: MS-DOS
(D) SOFTWARE: Wordperfect 5.1
- (vi) CURRENT APPLICATION DATA:
(A) APPLICATION NUMBER: NEW
(B) FILING DATE: December 12, 2000
(C) CLASSIFICATION:
- (vi) PRIOR APPLICATION DATA:
(A) APPLICATION NUMBER: 09/000,041
(B) FILING DATE: February 20, 1998
(C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:
(A) APPLICATION NUMBER: PCT/JP96/01956
(B) FILING DATE: July 12, 1996
- (viii) ATTORNEY/AGENT INFORMATION:
(A) NAME: Lee Cheng
(B) REGISTRATION NUMBER: 40,949
(C) REFERENCE/DOCKET NUMBER:
- (ix) TELECOMMUNICATION INFORMATION:
(A) TELEPHONE: 202-721-8200
(B) TELEFAX: 202-721-8250
(C) TELEX:

(2) INFORMATION FOR SEQ ID NO: 1:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 2116
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Human

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

GGCTCCTTAC CCACCCGGAG ACTTTTTTTT GAAAGGAAAC TAGGGAGGGAGGGAGAGGGA	60
GAGAGGGAGA AAACGAAGGG GAGCTCGTCC ATCCATTGAA GCACAGTTCA CT ATG	115
	Met
	1
ATC TTA CTC ACA TTC AGC ACT GGA AGA CGG TTG GAT TTC GTG CAT CAT	163
Ile Leu Leu Thr Phe Ser Thr Gly Arg Arg Leu Asp Phe Val His His	
	5 10 15
TCG GGG GTG TTT TTC TTG CAA ACC TTG CTT TGG ATT TTA TGT GCT ACA	211
Ser Gly Val Phe Phe Leu Gln Thr Leu Leu Trp Ile Leu Cys Ala Thr	
	20 25 30
GTC TGC GGA ACG GAG CAG TAT TTC AAT GTG GAG GTT TGG TTA CAA AAG	259
Val Cys Gly Thr Glu Gln Tyr Phe Asn Val Glu Val Trp Leu Gln Lys	
	35 40 45
TAC GGC TAC CTT CCA CCG ACT GAC CCC AGA ATG TCA GTG CTG CGC TCT	307
Tyr Gly Tyr Leu Pro Pro Thr Asp Pro Arg Met Ser Val Leu Arg Ser	
	50 55 60 65
GCA GAG ACC ATG CAG TCT GCC CTA GCT GCC ATG CAG CAG TTC TAT GGC	355
Ala Glu Thr Met Gln Ser Ala Leu Ala Ala Met Gln Gln Phe Tyr Gly	
	70 75 80
ATT AAC ATG ACA GGA AAA GTG GAC AGA AAC ACA ATT GAC TGG ATG AAG	403
Ile Asn Met Thr Gly Lys Val Asp Arg Asn Thr Ile Asp Trp Met Lys	
	85 90 95
AAG CCC CGA TGC GGT GTA CCT GAC CAG ACA AGA GGT AGC TCC AAA TTT	451
Lys Pro Arg Cys Gly Val Pro Asp Gln Thr Arg Gly Ser Ser Lys Phe	
	100 105 110
CAT ATT CGT CGA AAG CGA TAT GCA TTG ACA GGA CAG AAA TGG CAG CAC	499
His Ile Arg Arg Lys Arg Tyr Ala Leu Thr Gly Gln Lys Trp Gln His	
	115 120 125
AAG CAC ATC ACT TAC AGT ATA AAG AAC GTA ACT CCA AAA GTA GGA GAC	547
Lys His Ile Thr Tyr Ser Ile Lys Asn Val Thr Pro Lys Val Gly Asp	
	130 135 140 145
CCT GAG ACT CGT AAA GCT ATT CGC CGT GCC TTT GAT GTG TGG CAG AAT	595
Pro Glu Thr Arg Lys Ala Ile Arg Arg Ala Phe Asp Val Trp Gln Asn	
	150 155 160
GTA ACT CCT CTG ACA TTT GAA GAA GTT CCC TAC AGT GAA TTA GAA AAT	643
Val Thr Pro Leu Thr Phe Glu Glu Val Pro Tyr Ser Glu Leu Glu Asn	
	165 170 175

GGC Gly	AAA Lys	CGT Arg 180	GAT Asp	GTG Val	GAT Asp	ATA Ile	ACC Thr 185	ATT Ile	ATT Ile	TTT Phe	GCA Ala	TCT Ser 190	GGT Gly	TTC Phe	CAT His	691
GGG Gly	GAC Asp 195	AGC Ser	TCT Ser	CCC Pro	TTT Phe 200	GAT Asp	GGA Gly	GAG Glu	GGA Gly	GGA Gly	TTT Phe 205	TTG Leu	GCA Ala	CAT His	GCC Ala	739
TAC Tyr 210	TTC Phe	CCT Pro	GGA Gly	CCA Pro	GGA Gly 215	ATT Ile	GGA Gly	GGA Gly	GAT Asp	ACC Thr 220	CAT His	TTT Phe	GAC Asp	TCA Ser	GAT Asp 225	787
GAG Glu	CCA Pro	TGG Trp	ACA Thr	CTA Leu 230	GGA Gly	AAT Asn	CCT Pro	AAT Asn	CAT His 235	GAT Asp	GGA Gly	AAT Asn	GAC Asp	TTA Leu 240	TTT Phe	835
CTT Leu	GTA Val	GCA Ala	GTC Val 245	CAT His	GAA Glu	CTG Leu	GGA Gly	CAT His 250	GCT Ala	CTG Leu	GGA Gly	TTG Leu	GAG Glu 255	CAT His	TCC Ser	883
AAT Asn	GAC Asp	CCC Pro 260	ACT Thr	GCC Ala	ATC Ile	ATG Met	GCT Ala 265	CCA Pro	TTT Phe	TAC Tyr	CAG Gln	TAC Tyr 270	ATG Met	GAA Glu	ACA Thr	931
GAC Asp	AAC Asn 275	TTC Phe	AAA Lys	CTA Leu	CCT Pro	AAT Asn 280	GAT Asp	GAT Asp	TTA Leu	CAG Gln	GGC Gly 285	ATC Ile	CAG Gln	AAA Lys	ATA Ile	979
TAT Tyr 290	GGT Gly	CCA Pro	CCT Pro	GAC Asp	AAG Lys 295	ATT Ile	CCT Pro	CCA Pro	CCT Pro	ACA Thr 300	AGA Arg	CCT Pro	CTA Leu	CCG Pro	ACA Thr 305	1027
GTG Val	CCC Pro	CCA Pro	CAC His 310	CGC Arg	TCT Ser	ATT Ile	CCT Pro	CCG Pro	GCT Ala 315	GAC Asp	CCA Pro	AGG Arg	AAA Lys	AAT Asn 320	GAC Asp	1075
AGG Arg	CCA Pro	AAA Lys	CCT Pro 325	CCT Pro	CGG Arg	CCT Pro	CCA Pro	ACC Thr 330	GGC Gly	AGA Arg	CCC Pro	TCC Ser	TAT Tyr 335	CCC Pro	GGA Gly	1123
GCC Ala	AAA Lys	CCC Pro 340	AAC Asn	ATC Ile	TGT Cys	GAT Asp	GGG Gly 345	AAC Asn	TTT Phe	AAC Asn	ACT Thr	CTA Leu	GCT Ala 350	ATT Ile	CTT Leu	1171
CGT Arg	CGT Arg	GAG Glu 355	ATG Met	TTT Phe	GTT Val	TTC Phe 360	AAG Lys	GAC Asp	CAG Gln	TGG Trp	TTT Phe 365	TGG Trp	CGA Arg	GTG Val	AGA Arg	1219
AAC Asn 370	AAC Asn	AGG Arg	GTG Val	ATG Met	GAT Asp 375	GGA Gly	TAC Tyr	CCA Pro	ATG Met	CAA Gln	ATT Ile	ACT Thr	TAC Tyr	TTC Phe	TGG Trp 385	1267
CGG Arg	GGC Gly	TTG Leu	CCT Pro	CCT Pro	AGT Ser 390	ATC Ile	GAT Asp	GCA Ala	GTT Val 395	TAT Tyr	GAA Glu	AAT Asn	AGC Ser	GAC Asp	GGG Gly	1315

AAAT Asn	TTT Phe	GTG Val	TTC Phe	TTT Phe	AAA Lys	GGT Gly	AAC Asn	AAA Lys	TAT Tyr	TGG Trp	GTG Val	TTC Phe	AAG Lys	GAT Asp	ACA Thr	1363
405410415																
ACT Thr	CTT Leu	CAA Gln	CCT Pro	GGT Gly	TAC Tyr	CCT Pro	CAT His	GAC Asp	TTG Leu	ATA Ile	ACC Thr	CTT Leu	GGA Gly	AGT Ser	GGA Gly	1411
420425430																
ATT Ile	CCC Pro	CCT Pro	CAT His	GGT Gly	ATT Ile	GAT Asp	TCA Ser	GCC Ala	ATT Ile	TGG Trp	TGG Trp	GAG Glu	GAC Asp	GTC Val	GGG Gly	1459
435440445																
AAA Lys	ACC Thr	TAT Tyr	TTC Phe	TTC Phe	AAG Lys	GGA Gly	GAC Asp	AGA Arg	TAT Tyr	TGG Trp	AGA Arg	TAT Tyr	AGT Ser	GAA Glu	GAA Glu	1507
450455460465																
ATG Met	AAA Lys	ACA Thr	ATG Met	GAC Asp	CCT Pro	GGC Gly	TAT Tyr	CCC Pro	AAG Lys	CCA Pro	ATC Ile	ACA Thr	GTC Val	TGG Trp	AAA Lys	1555
470475480																
GGG Gly	ATC Ile	CCT Pro	GAA Glu	TCT Ser	CCT Pro	CAG Gln	GGA Gly	GCA Ala	TTT Phe	GTA Val	CAC His	AAA Lys	GAA Glu	AAT Asn	GGC Gly	1603
485490495																
TTT Phe	ACG Thr	TAT Tyr	TTC Phe	TAC Tyr	AAA Lys	GGA Gly	AAG Lys	GAG Glu	TAT Tyr	TGG Trp	AAA Lys	TTC Phe	AAC Asn	AAC Asn	CAG Gln	1651
500505510																
ATA Ile	CTC Leu	AAG Lys	GTA Val	GAA Glu	CCT Pro	GGA Gly	CAT His	CCA Pro	AGA Arg	TCC Ser	ATC Ile	CTC Leu	AAG Lys	GAT Asp	TTT Phe	1699
515520525																
ATG Met	GGC Gly	TGT Cys	GAT Asp	GGA Gly	CCA Pro	ACA Thr	GAC Asp	AGA Arg	GTT Val	AAA Lys	GAA Glu	GGA Gly	CAC His	AGC Ser	CCA Pro	1747
530535540545																
CCA Pro	GAT Asp	GAT Asp	GTA Val	GAC Asp	ATT Ile	GTC Val	ATC Ile	AAA Lys	CTG Leu	GAC Asp	AAC Asn	ACA Thr	GCC Ala	AGC Ser	ACT Thr	1795
550555560																
GTG Val	AAA Lys	GCC Ala	ATA Ile	GCT Ala	ATT Ile	GTC Val	ATT Ile	CCC Pro	TGC Cys	ATC Ile	TTG Leu	GCC Ala	TTA Leu	TGC Cys	CTC Leu	1843
565570575																
CTT Leu	GTA Val	TTG Leu	GTT Val	TAC Tyr	ACT Thr	GTG Val	TTC Phe	CAG Gln	TTC Phe	AAG Lys	AGG Arg	AAA Lys	GGA Gly	ACA Thr	CCC Pro	1891
580585590																
CGC Arg	CAC His	ATA Ile	CTG Leu	TAC Tyr	TGT Cys	AAA Lys	CGC Arg	TCT Ser	ATG Met	CAA Gln	GAG Glu	TGG Trp	GTG Val	TGATGTAGG		1942
595600605																
GTTTTTTTCTT CTTTCTTTCT TTTGCAGGAG TTTGTGGTAA CTTGAGATTTC AAGACAAGAG 2002																
CTGTTATGCT GTTTCCTAGC TAGGAGCAGG CTTGTGGCAG CCTGATTCGG GGCTGACCTT 2062																
TCAAACCAGA GGGTTGCTGG TCCTGCACAT GAGTGGAAAT ACACTCATGG GGAA 2116																

(i) SEQUENCE CHARACTERISTICS:

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

Met 1	Ile	Leu	Leu	Thr 5	Phe	Ser	Thr	Gly	Arg 10	Arg	Leu	Asp	Phe	Val 15	His
His	Ser	Gly	Val 20	Phe	Phe	Leu	Gln	Thr 25	Leu	Leu	Trp	Ile	Leu 30	Cys	Ala
Thr	Val	Cys 35	Gly	Thr	Glu	Gln	Tyr 40	Phe	Asn	Val	Glu	Val 45	Trp	Leu	Gln
Lys	Tyr 50	Gly	Tyr	Leu	Pro	Pro 55	Thr	Asp	Pro	Arg	Met 60	Ser	Val	Leu	Arg
Ser 65	Ala	Glu	Thr	Met	Gln 70	Ser	Ala	Leu	Ala	Ala 75	Met	Gln	Gln	Phe	Tyr 80
Gly	Ile	Asn	Met	Thr 85	Gly	Lys	Val	Asp	Arg 90	Asn	Thr	Ile	Asp	Trp 95	Met
Lys	Lys	Pro	Arg 100	Cys	Gly	Val	Pro	Asp 105	Gln	Thr	Arg	Gly	Ser 110	Ser	Lys
Phe	His	Ile 115	Arg	Arg	Lys	Arg	Tyr 120	Ala	Leu	Thr	Gly	Gln 125	Lys	Trp	Gln
His 130	Lys	His	Ile	Thr	Tyr 135	Ser	Ile	Lys	Asn	Val	Thr 140	Pro	Lys	Val	Gly
Asp 145	Pro	Glu	Thr	Arg	Lys 150	Ala	Ile	Arg	Arg	Ala 155	Phe	Asp	Val	Trp	Gln 160
Asn	Val	Thr	Pro	Leu 165	Thr	Phe	Glu	Glu	Val 170	Pro	Tyr	Ser	Glu	Leu 175	Glu
Asn	Gly	Lys	Arg 180	Asp	Val	Asp	Ile	Thr 185	Ile	Ile	Phe	Ala	Ser 190	Gly	Phe
His	Gly 195	Asp	Ser	Ser	Pro	Phe	Asp 200	Gly	Glu	Gly	Gly	Phe 205	Leu	Ala	His
Ala	Tyr	Phe	Pro	Gly	Pro	Gly	Ile	Gly	Gly	Asp	Thr	His	Phe	Asp	Ser

	210				215				220						
Asp 225	Glu	Pro	Trp	Thr	Leu 230	Gly	Asn	Pro	Asn	His 235	Asp	Gly	Asn	Asp	Leu 240
Phe	Leu	Val	Ala	Val 245	His	Glu	Leu	Gly	His 250	Ala	Leu	Gly	Leu	Glu	His
Ser	Asn	Asp	Pro 260	Thr	Ala	Ile	Met	Ala 265	Pro	Phe	Tyr	Gln	Tyr 270	Met	Glu
Thr	Asp	Asn 275	Phe	Lys	Leu	Pro	Asn 280	Asp	Asp	Leu	Gln	Gly 285	Ile	Gln	Lys
Ile	Tyr 290	Gly	Pro	Pro	Asp	Lys 295	Ile	Pro	Pro	Pro	Thr 300	Arg	Pro	Leu	Pro
Thr 305	Val	Pro	Pro	His	Arg 310	Ser	Ile	Pro	Pro	Ala 315	Asp	Pro	Arg	Lys	Asn 320
Asp	Arg	Pro	Lys	Pro 325	Pro	Arg	Pro	Pro	Thr 330	Gly	Arg	Pro	Ser	Tyr 335	Pro
Gly	Ala	Lys	Pro 340	Asn	Ile	Cys	Asp	Gly 345	Asn	Phe	Asn	Thr	Leu 350	Ala	Ile
Leu	Arg	Arg 355	Glu	Met	Phe	Val	Phe 360	Lys	Asp	Gln	Trp	Phe 365	Trp	Arg	Val
Arg	Asn 370	Asn	Arg	Val	Met	Asp 375	Gly	Tyr	Pro	Met	Gln 380	Ile	Thr	Tyr	Phe
Trp 375	Arg	Gly	Leu	Pro 390	Pro	Ser	Ile	Asp	Ala 395	Val	Tyr	Glu	Asn	Ser	Asp 400
Gly	Asn	Phe	Val	Phe 405	Phe	Lys	Gly	Asn	Lys 410	Tyr	Trp	Val	Phe	Lys 415	Asp
Thr	Thr	Leu	Gln 420	Pro	Gly	Tyr	Pro	His 425	Asp	Leu	Ile	Thr	Leu 430	Gly	Ser
Gly	Ile	Pro 435	Pro	His	Gly	Ile	Asp 440	Ser	Ala	Ile	Trp	Trp 445	Glu	Asp	Val
Gly	Lys 450	Thr	Tyr	Phe	Phe	Lys 455	Gly	Asp	Arg	Tyr	Trp 460	Arg	Tyr	Ser	Glu
Glu 465	Met	Lys	Thr	Met	Asp 470	Pro	Gly	Tyr	Pro	Lys 475	Pro	Ile	Thr	Val	Trp 480
Lys	Gly	Ile	Pro	Glu 485	Ser	Pro	Gln	Gly	Ala 490	Phe	Val	His	Lys	Glu 495	Asn
Gly	Phe	Thr 500	Tyr	Phe	Tyr	Lys	Gly	Lys 505	Glu	Tyr	Trp	Lys 510	Phe	Asn	Asn
Gln	Ile	Leu	Lys	Val	Glu	Pro	Gly	His	Pro	Arg	Ser	Ile	Leu	Lys	Asp

(2) INFORMATION FOR SEQ ID NO: 3:

(A) LENGTH: 20
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

20

(2) INFORMATION FOR SEQ ID NO: 4:

(A) LENGTH: 27
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

27

(2) INFORMATION FOR SEQ ID NO: 5:

(A) LENGTH: 14
(B) TYPE: Amino acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:

(2) INFORMATION FOR SEQ ID NO: 6:

(ii) MOLECULE TYPE: Peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:

(2) INFORMATION FOR SEQ ID NO: 7:

(ii) MOLECULE TYPE: Peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:

Ser Ala

(2) INFORMATION FOR SEQ ID NO: 8:

(ii) MOLECULE TYPE: Peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:

Thr Leu Gly Asn Pro Asn His Asp Gly Asn Asp Leu Phe Leu
1 5 10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9:

(2) INFORMATION FOR SEQ ID NO: 10:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 10:

(2) INFORMATION FOR SEQ ID NO: 11:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 11:

(2) INFORMATION FOR SEQ ID NO: 12:

```
(i) SEQUENCE CHARACTERISTICS:
      (A) LENGTH:          7
      (B) TYPE:            Amino acid
      (D) STRANDEDNESS:    Single
      (C) TOPOLOGY:        Linear
```

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 12:

(2) INFORMATION FOR SEQ ID NO: 13:

(ii) MOLECULE TYPE: Peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 13:

(2) INFORMATION FOR SEQ ID NO: 14:

(ii) MOLECULE TYPE: Peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 14:

Arg Xaa Lys Arg
1